(1) Claims Objections - Wording informalities in the claims

Claims 24-43 have been revised according to the Examiner's instructions to overcome the objection because of informalities.

(2) Claims Rejections – 35 USC § 112 – Written Description

In rejecting claims 23-43 based on the written description, the Examiner said the "claims are broadly drawn to a method for transferring any trait of interest into a maize plant wherein said trait is associated with one or more molecular markers." However, the specification and claims describe a series of novel alleles formed in intergeneric hybrids between *Tripsacum* sp. and teosinte that are identified by their unique molecular weights as detected by specific RFLP probe-restriction enzyme combinations. In maize, the RFLP markers detect three or four alleles at each genetic locus in an easily interpretable pattern across a variety of inbred maize lines (Gardiner et al. 1993, p. 925). Construction of the molecular marker map was possible because each maize parent contributes its particular allele as detected by each enzyme-probe combination to the F_1 hybrid progeny produced by crossing two maize inbred lines. Then the inheritance of the alleles detected by the RFLP markers was followed in large, segregating F_2 and F_3 generations, and recombination frequencies analyzed statistically by linear regression and other statistical programs to project probabilities of association of probes with genetic loci on the ten maize linkage groups. Based on the molecular marker map in maize, the genetic concept of this application does not follow what one skilled in the art would have predicted. Rather than inheriting an allele from each parent, the progeny of crosses between *Tripsacum* and teosinte exhibit novel alleles formed by recombination of their distinctive genomes. These novel alleles are visualized as bands on autoradiographs and are precisely described by their molecular weight and specific probe-enzyme combination. The genetic material disclosed herein is unprecedented in the plant literature and would **not** have been obvious to one skilled in the art of genetics and plant breeding. As stated in the specification, page 20, paragraph 1, "Such mutant or novel rearrangements in the genetic material are revealed by comparative analysis of the RFLP bands of the parent plants and hybrid progeny. Bands present in the offspring not found in either parent indicate regions of the genome where novel genetic material has arisen, i.e. mutations have

occurred...In addition to the rarity and usual deleterious effect of mutations, a basic biological tenet is that mutations occur at random or by chance (Lewin 1997). In a study of spontaneous mutation rates to new length alleles at tandemly repeated loci in human DNA (Jeffreys et al. 1988) mutations arose sporadically and there was no clustering of mutations within a family. Siblings never shared a common mutant allele. Therefore, it is unexpected that the same unique polymorphisms are repeatedly found in hybrid progeny derived from crossing different *Tripsacum* and different teosinte parent plants..."

Examples of how to identify molecular markers that co-segregate with two traits were provided in the specification to illustrate precisely how easily and quickly one skilled in the art can identify the novel allele or alleles associated with a particular probe-enzyme combination that co-segregates with an agronomic trait. This process does not require undue experimentation and complex statistical analyses of large populations over multiple generations as required for maize molecular mapping. Comparative genomic analysis using Tables 2 and 3 of the specification would enable anyone skilled in the art to rapidly detect which novel alleles are associated with a trait by examining a single generation of a small, segregating population of 8 to 24 plants in which some plants express the trait and others do not. First, to identify an initial set of candidate alleles associated with the trait, you eliminate all of the novel alleles that are shared in plants that express the trait and plants that do not express the trait. Then you further narrow down the pool of candidate alleles by comparing the remaining alleles among the plants that express the trait to only those alleles that are shared by all the plants expressing the trait. Next, you compare the alleles to those of the *Tripsacum*-teosinte progenitor plant expressing the trait with recombinant lines in Tables 2 and 3, distinguishing between those recombinants that also express the trait and those that do not to complete the identification of which novel candidate alleles co-segregate with the trait. Thus, the novel alleles from the *Tripsacum*-teosinte recombinants provide a new method of genetic analysis that bypasses the complicated, extensive experimentation and statistical analyses required to construct a molecular marker linkage map from multiple generations of large breeding populations. As stated in the specification last paragraph, starting line 6, page 23, continuing on page 24: "The unique *Tripsacum* polymorphisms and recombinant chimeric RFLPs, their heritability in succeeding generations of *Tripsacum*-teosinte hybrids, and their transmissibility to maize is unprecedented and unexpected based on prior art. These novel DNA fragments have utility for genetic analysis of *Zea*, and

selection of new variant alleles that may enhance traits such as insect and disease resistance, drought stress tolerance, cold tolerance, herbicide tolerance, perennialism, increased grain yield, totipotency, apomixis, better root systems, tolerance of water-logged soils, tolerance of high-aluminum and acidic soils, improved grain quality, and improved forage quality. When these novel RFLPs co-segregate with crop improvement traits, they can be successfully employed in recurrent selection breeding programs for early and rapid screening of plants carrying the desired trait."

The specification describes a new method to identify unique alleles introgressed from a *Tripsacum*-teosinte parent into maize, and it describes a method of rapid genetic analysis how to determine if one or more of the novel alleles co-segregates with an agronomoic trait. Traits in the claims and specification are traits known in *Tripsacum* and/or traits observed in the Applicant's recurrent selection breeding program. For example in the specification on page 7, paragraph 3: "Feasibility has been demonstrated in plants derived from crossing *Tripsacum*-teosinte recombinants with maize that are resistant to corn rootworm (*Diabrotica* sp.) and corn borer, are drought tolerant, have properties of perennialism, develop aerenchyma tissue in their roots, and can grow in low pH conditions. Investigation and characterization of other improvements to maize including herbicide tolerance, aflatoxin resistance, and enhanced grain quality are underway."

In regard to claims 28-31 and 33-43, page 4, paragraph 1 of the Final Office Action, November 29, 2006, the Examiner states: "there does not appear to be literal support in the specification for plants with the claimed characteristics." Although the Examiner has directed the claims to NEW MATTER, each trait mentioned in the claims is described in the specification. Annotation of where support for each trait can be found in the specification per each claim (currently amended) is provided as follows:

Claim 28 (Currently amended). [The] <u>A</u> plant <u>identified</u> according to <u>the method of</u> claim 23 or <u>produced according to</u> claim 25, whereby said plant has improved grain quality.

In the specification: on page 1, paragraph 1, lines 13-24 – "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for… transfer of new genes in corn improvement that confer… improved grain quality" – on page 7, paragraph 3, lines 1-7 – "Investigation and characterization of other improvements to maize including…enhanced grain quality are underway." - on page 14, paragraph

1, lines 4-7 – "...these plants may contain novel genes for such traits as...improved grain quality..." – on page 23, paragraph 3, lines 10-11, continuing on page 24, lines 1-5 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...improved grain quality..."

Claim 29 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25, whereby said plant is tolerant of acid soils.

In the specification: on page 1, paragraph 1, lines13-23 – "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for... transfer of new genes in corn improvement that confer... tolerance of high aluminum and acidic soils" – on page 7, paragraph 3, lines 1-5 – " Feasibility has been demonstrated in plants derived from crossing *Tripsacum*-teosinte recombinants with maize that...can grow in low pH conditions." - on page 14, paragraph 1, lines 4-7 – "...these plants may contain novel genes for such traits as...tolerance to acidic soils..." – page 23, paragraph 3, lines 10-11, continuing to page 24, lines 4-5 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...tolerance of high aluminum and acidic soils..." – on page 27, lines 10-11 – "Since subsoils are highly acidic, aerenchyma appears to be associated with gamagrass' strong aluminum tolerance (Clark et al. 1996; Foy 1997)."

Claim 30 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25, whereby said plant is resistant to aflatoxin.

In the specification: on page 7, paragraph 3, lines 1-7 – " Feasibility has been demonstrated in plants derived from crossing *Tripsacum*-teosinte recombinants with maize...Investigation and characterization of other improvements to maize including...aflatoxin resistance...are underway."

Claim 31 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25, whereby said plant is resistant to corn borer.

In the specification: on page 7, paragraph 3, lines 1-3 – " Feasibility has been demonstrated in plants derived from crossing *Tripsacum*-teosinte recombinants with maize that are resistant to...corn borer..."

Claim 33 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25, whereby said plant tolerates saturated soils.

In the specification: on page 1, paragraph 1, lines 13-23 – "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for... transfer of new genes in corn improvement that confer... tolerance of water-logged soils" - on page 14, paragraph 1, lines 4-6 – "...these plants may contain novel genes for such traits as...water-logging tolerance..." – on page 23, paragraph 3, lines 10-11, continuing to page 24, line 4 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...tolerance of water-logged soils..." – on page 27, lines 5-8 – "The roots of *Tripsacum dactyloides* possess constitutive aerenchyma (Ray et al. 1998). The air-filled passages in the roots enable gamagrass to grow in saturated soils and to penetrate compacted layers so it can tolerate both floods and droughts (Clark et al. 1996; Foy 1996; Ray et al. 1998)."

Claim 34 (Currently amended). [The] <u>A</u> plant <u>identified</u> according to <u>the method of</u> claim 23 or <u>produced according to claim</u> 25, whereby said plant is resistant to aluminum toxicity.

In the specification: on page 1, paragraph 1, lines13-23 – "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for... transfer of new genes in corn improvement that confer... tolerance of high aluminum and acidic soils" - on page 14, paragraph 1, lines 4-7 – "...these plants may contain novel genes for such traits as...tolerance to high-aluminum soils..." – on page 23, paragraph 3, lines 10-11, continuing to page 24, lines 4-5 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...tolerance of high aluminum and acidic soils..." – on page 27, lines 10-11 – "Since subsoils are highly acidic, aerenchyma appears to be associated with gamagrass' strong aluminum tolerance (Clark et al. 1996; Foy 1997)."

Claim 35 (Currently amended). [The] <u>A</u> plant <u>identified</u> according to <u>the method of</u> claim 23 or <u>produced according to claim</u> 25, whereby said plant is drought tolerant.

In the specification: on page 1, paragraph 1, lines13-20 – "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for assisting selection of desirable traits in maize breeding programs, for detection of target DNA sequences in genetic analyses, and for the identification and transfer of new genes in corn improvement that confer... drought stress tolerance..." – on page 7, paragraph 3, lines 1-3 – " Feasibility has been demonstrated in plants derived from crossing *Tripsacum*-teosinte recombinants with maize that...are drought tolerant." - on page 14,

paragraph 1, lines 4-7 – "...these plants may contain novel genes for such traits as...drought tolerance..." – on page 23, paragraph 3, lines 10-11, continuing to page 24, lines 1-2 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...drought stress tolerance..." – on page 27, lines 5-10 – "The roots of *Tripsacum dactyloides* possess constitutive aerenchyma (Ray et al. 1998). The air-filled passages in the roots enable gamagrass to grow in saturated soils and to penetrate compacter layers so it can tolerate both floods and droughts (Clark et al. 1996; Foy 1996; Ray et al. 1998). The roots can grow deep into subsoils to tap water reserves." – on page 27, paragraph 1, lines 7-11, continuing on page 28, through line 5 – "In a population of 24 SDG058 plants in a breeding program selecting for strong drought tolerance, all had aerenchyma...Fifteen had well developed aerenchyma indicating they are homozygous for the trait. Roots of plants from three other (*Tripsacum*-teosinte X maize) hybrid lines that were not selected for drought tolerance (9094 X 7009, 00-2-17, and 99-16-3 did not develop aerenchyma. This confirms that the presence of root aerenchyma is contributing to drought tolerance in line SDG058.

Claim 36 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25 further comprising a novel band identified by SSR probe phi123, SSR probe bnlg2235, SSR probe bnlg1714, SSR probe bnlg1805, or SSR probe dupSSR23, thereof. **In the specification**: on page 26, lines 12-19, - "In addition to producing distinct polymorphisms that were inherited from both the *Tripsacum* and *Zea* parents, novel SSR bands were also observed in the *Tripsacum*-teosinte recombinants and crosses between *Tripsacum*-teosinte hybrids and maize. SSR markers that map to the same genetic loci as the RFLP markers employed to fingerprint the *Tripsacum*-teosinte hybrids are listed in Table 5 and indicated beneath each corresponding RFLP marker in Fig. 2." – on page 29, paragraph 2 – The present invention provides a method for marker assisted selection of plants...by the presence of unique DNA fragments revealed by...their SSR markers bnlg2235, dupSSR23, phi123 and bnlg1714, respectively." – on page 29, paragraph 3, continuing on page 30 – "The present invention provides a method for marker assisted selection of plants...by the presence of a unique DNA fragment revealed by...SSR marker bnlg1805."

Claim 37 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25, whereby said plant has tolerance to low nitrogen.

In the specification: on page 1, paragraph 1, lines 13-25 – "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.)

provide unique markers for assisting selection of desirable traits in maize breeding programs, for detection of target DNA sequences in genetic analyses, and for the identification and transfer of new genes in corn improvement that confer...ability to attract nitrogen-fixing bacteria to the rhizophere..." – on page 14, paragraph 1, lines 4-11 – "...these plants may contain novel genes for such traits as...and ability to attract nitrogen-fixing bacteria to the rhizosphere."

Claim 38 (Currently amended). [The] <u>A</u> plant <u>identified</u> according to <u>the method of</u> claim 23 or <u>produced according to</u> claim 25, whereby said plant exhibits apomixis.

In the specification: on page 1, paragraph 1, lines13-21 - "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for assisting selection of desirable traits in maize breeding programs, for detection of target DNA sequences in genetic analyses, and for the identification and transfer of new genes in corn improvement that confer...apomixis..." – on page 23, paragraph 3, lines 10-11, continuing to page 24, lines 1-3 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...apomixis..."

Claim 39 (Currently amended). [The] <u>A</u> plant <u>identified</u> according to <u>the method of</u> claim 23 or <u>produced according to</u> claim 25, whereby said plant is cold tolerant.

In the specification: on page 1, paragraph 1, lines 13-20 - "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for assisting selection of desirable traits in maize breeding programs, for detection of target DNA sequences in genetic analyses, and for the identification and transfer of new genes in corn improvement that confer...cold tolerance..." – on page 23, paragraph 3, lines 10-11, continuing to page 24, lines 1-2 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...cold tolerance,..."

Claim 40 (Currently amended). [The] <u>A</u> plant <u>identified</u> according to <u>the method of</u> claim 23 or <u>produced according to</u> claim 25, whereby said plant has improved forage quality.

In the specification: on page 1, paragraph 1, lines 13-24 - "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for assisting selection of desirable traits in maize breeding programs, for detection of target DNA sequences in genetic analyses, and for the identification and transfer of new genes in corn improvement that confer...enhanced forage quality..." – on page 14, paragraph 1, lines 4-7 – "...these plants may contain novel genes for such traits

as...improved forage quality..." – on page 23, paragraph 3, lines 10-11, continuing to page 24 lines 1-5 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...and improved forage quality."

Claim 41 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25, whereby said plant has more extensive, robust roots.

In the specification: on page 1, paragraph 1, lines 13-21 - "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for assisting selection of desirable traits in maize breeding programs, for detection of target DNA sequences in genetic analyses, and for the identification and transfer of new genes in corn improvement that confer...improved root systems..." – on page 23, paragraph 3, lines 10-11, continuing to page 24, lines 1-3 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...better root systems...."

Claim 42 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25, whereby said plant exhibits totipotency.

In the specification: on page 1, paragraph 1, lines 13-21 - "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for assisting selection of desirable traits in maize breeding programs, for detection of target DNA sequences in genetic analyses, and for the identification and transfer of new genes in corn improvement that confer...totipotency..." – on page 23, paragraph 3, lines 10-11, continuing to page 24, lines 1-3 – "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...totipotency...."

Claim 43 (Currently amended). [The] A plant identified according to the method of claim 23 or produced according to claim 25, whereby said plant exhibits perennialism.

In the specification: on page 1, paragraph 1, lines 13-20 - "These variant DNA fragments formed as a result of intergeneric hybridization between gamagrass (*Tripsacum* sp.) and teosinte (*Zea* sp.) provide unique markers for assisting selection of desirable traits in maize breeding programs, for detection of target DNA sequences in genetic analyses, and for the identification and transfer of new genes in corn improvement that confer...perennialism..." – on page 7, paragraph 3, lines 1-4 – " Feasibility has been demonstrated in plants derived from crossing *Tripsacum*-teosinte recombinants with maize that...have properties of perennialism..." – on page

14, paragraph 1, lines 4-7 – "...these plants may contain novel genes for such traits as...totipotency..." – on page 23, paragraph 3, lines 10-11, continuing to page 24 lines 1-2"– "These novel DNA fragments have utility for...selection of new variant alleles that may enhance traits such as ...perennialism...."

As described in detail above, the novel alleles from the *Tripsacum*-teosinte recombinants provide a new method of genetic analysis that bypasses the long, drawn-out experimentation of marker-assisted maize breeding for trait selection. Anyone skilled in the art can easily and quickly compare the banding patterns of *Tripsacum* X teosinte plants, teosinte X *Tripsacum* plants, *Tripsacum*-teosinte X maize plants, or teosinte-Tripsacum X maize plants with a trait to recombinant plants that do not express the same trait and determine which novel alleles are associated with the trait by visual analysis and a simple process of elimination. Therefore, the written description of the invention does provide definition of a new method for genetic analysis that clearly distinguishes the claimed subject matter from other materials. The detailed descriptions of the novel alleles by molecular weights and associated probe-enzyme combinations and its presentation in tabular format (cf. Tables 2 and 3) make it easy to discern the novel allelelic patterns and thus "visualize or recognize the identity of the members of the genus." This is in accordance with the ruling in University of California v. Eli Lily and Co, 119 F. 3d 1559, 1568; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997) (ref. Examiner's comments, page 6, paragraph 1, Final Office Action).

The characteristics in claims 28-31 and 33-43 have been described in the specification according to the annotations by page, paragraph, and line numbers for each trait claimed as provided above. This demonstrates the Applicant was in possession of the claimed invention. Using the new method of genetic analysis provided in the specification with the process of how to employ it for identification of a novel allele and a co-segregating agronomic trait, anyone skilled in the art would be able to quickly and easily determine a novel allele-trait association. Specific examples illustrating precisely how to do this are provided in the written description on pages 24-29 of the specification.

(3) Claims Rejections - Enablement – 35 USC § 112

On page 8, paragraph 2, Final Office Action, November 29, 2006, the Examiner argues: "The claims are broadly drawn to a method for transferring any trait of intearest into a maize

plant wherein said trait is associated with one or more molecular markers." The Applicant respectfully argues that this application is **not** "broadly drawn to a method for transferring any trait of interest into a maize plant wherein said trait is associated with one or more molecular markers." It is drawn to a method for identifying one or more unique alleles from an intergeneric cross between *Tripsacum* and teosinte that have been introgressed into maize. It further provides a method for quickly and easily identifying which of the novel alleles in claim 23 are associated with an agronomic trait. As pointed out above, all direction and guidance necessary for one skilled in the art, along with working examples of the invention, are clearly and thoroughly described in the specification. Any viable cross between *Tripsacum* and teosinte results from precise genomic rearrangements that produce many of the same unique recombinant alleles in progeny from said crosses, regardless of which *Tripsacum* sp. is used in the cross. The replicability, genomic stability, and reliable heritability of these novel alleles have been demonstrated in crosses between different *Tripsacum* sp. and teosinte parents from different plant populations. Anyone skilled in the art can make a cross between a *Tripsacum* sp. and teosinte as described in the specification on pages 30-31, and they will recover recombinant plants that contain a number of the same novel alleles in claim 23 and described in the specification (Tables 2 and 3). Anyone skilled in the art can cross those plants with maize as described on page 31 of the specification, and the progeny will contain one or more of the novel alleles in claim 23 and Tables 2 and 3 of the specification. As described above, a simple process of comparing the banding patterns of the novel alleles (i.e. molecular weights per probe-enzyme combination) in progeny expressing a particular trait to progeny that do not have the trait permits rapid detection of alleles that are associated with the trait of interest. On page 11, paragraph 1, lines 3-5 of the Final Office Action, 11/29/06, the Examiner agreed: "The specification provides guidance and working examples regarding the claimed invention using RFLPs associated with corn rootworm resistance and aerenchyma."

The Examiner acknowledged receipt of the copy of the ATCC 75297 seed deposit (Page 11, paragraph 3 of the Final Office Action, 11/29/06), which was requested in the telephone interview on June 1, 2006 (Page 3, paragraph 4 of the Interview Summary, June 6, 2006). The Examiner stated the "deposit does not enable the method because the hybrid does not enable one skilled in the art to which markers are associated with specific traits. In addition, it does not enable the claimed plants (claims 23-43) because there is not evidence that the deposited line

possesses all of the characteristics of these plants." The ATCC 75297 deposit, made on August 28, 1992, was seed of a "*Tripsacum/Zea diploperennis* hybrid", i.e. it was seed of a cross between a *Tripsacum* female parent pollinated by a *Zea diploperennis* male parent. The seeds are from the plant referred to as Tripsacorn in the specification (page 22, paragraph 1, lines 16-17 and lines 24-32, page 23, line 1, page 24, last line, page 25, line 10, page 27, line 16 and paragraph 1, lines 4-10, page 28, paragraph 3, lines 1-7, Tables 2 and 3). The unique alleles present in Tripsacorn are provided in Tables 2 and 3 of the specification. The ATCC 75297 deposit was presented as documentation of one example of a cross between *Tripsacum* and teosinte. This invention broadly refers to any cross between *Tripsacum* sp. and teosinte. Examples of five other hybrids between *Tripsacum* sp. and teosinte are described in the specification on pages 22-25, pages 27-29, and in Tables 2 and 3. As explained in the preceding paragraph, in any crosses between *Tripsacum* sp. and teosinte, whether *Tripsacum* is the female parent or pollen donor in the cross, the same, precise genomic rearrangements that produce the same novel alleles in progeny from said crosses, regardless of which *Tripsacum* sp. is used in the cross, are formed. The replicability, genomic stability, and reliable heritability of these novel alleles have been demonstrated in crosses between different *Tripsacum* sp. and teosinte parents from different plant populations. Anyone skilled in the art can make a cross between *Tripsacum* sp. and teosinte as described in the specification on pages 30-31, and they will recover recombinant plants that contain a number of the same novel alleles presented in claim 23, in Tables 2 and 3, and elsewhere in the specification.

(4) Claims Rejections – 35 USC § 102

The Examiner rejected claims 24-27 under 35 USC § 102 as being anticipated by Eubanks (U.S. Patent 5,330,547, July 19, 1994). The Examiner argued (page 12, paragraph 2 of the Final Office Action, 11/29/06): 'Though Eubanks does not further screen the plant's DNA as stated in step (f), the plant would inherently possess the claimed restriction fragments because the plant was produced by the same method as the claimed invention." Eubanks (U.S. Patent 5,330,547) makes no reference to molecular markers, is silent as to the unique alleles described in this invention, and is restricted to a cross between a *Tripsacum* female parent and a teosinte pollen donor. As explained in the preceding paragraph, in any crosses between *Tripsacum* and teosinte, whether *Tripsacum* is the female parent or pollen donor in the cross, and regardless of

which *Tripsacum* sp. is used in the cross, the precise genomic rearrangements that produce the novel recombinant alleles in progeny from said crosses occur. The replicability, genomic stability, and reliable heritability of these novel alleles have been demonstrated in crosses between different *Tripsacum* and teosinte parents from different plant populations and geographical regions (progeny from different crosses in which teosinte was the female parent and in which the parents came from different species and divergent populations are described on pages 22-23 and 24-29 and in Tables 3 and 4 of the specification). Because these novel alleles defy everything we know about mutations, mutation frequencies, and heritability in siblings (see detailed discussion above and in the specification, pages 2-3 and page 20), it would **not** have been obvious to, or anticipated by, anyone one skilled in the art that a high frequency of novel recombinant alleles (i.e. mutations not found in either parent) would occur in progeny derived from crossing *Tripsacum* and teosinte. Nor would if have been obvious to or anticipated by anyone skilled in the art that the same novel recombinant alleles (i.e. mutations not found in either parent) would occur in progeny from crossing different *Tripsacum* sp. and teosinte plants from different populations and geographical regions. This is unprecedented in the literature, defies the conventional paradigm for allelic inheritance in genetics, and clearly establishes that the prior art would neither anticipate nor render obvious the claimed invention.

In accordance with M.P.E.P. Section 1504.06 concerning non-statutory, obviousness double-patenting, differences must be obvious to a designer of ordinary skill in the art related to the claimed design. If the reference does not fully disclose the narrower claim then a double-patenting rejection should not be made. "If the broader claim of the reference does not disclose the additional subject matter claimed in the narrower claim, then the applicant could not have claimed the narrower claim at the time the application with the broader claim was filed and a rejection under non-statutory double patenting of the differing scope-type would be inappropriate." (www.bitlaw.com/source/mpep/1504_06.html)

Claim 23 has been amended according to the Examiner's recommendation such that steps described in Eubanks (U.S. Patent 5,330,547) are no longer in the amended claim and the prior art rejection is no longer applicable. Resistance to corn rootworm, which was claimed in Eubanks (U.S. Patent 5,330,547), is not claimed in this application.

(5) New Claims Rejections – 35 USC § 102(b)

In the Final Office Action, November 29, 2006, page 13, item 14, the Examiner rejected claims 24-27 under 35 U.S.C. 102(b) as being anticipated by Eubanks (US Patent No. 5,750,828, May 12, 1998). Eubanks (U.S. Patent 5,750,828), makes no reference to molecular markers, and is silent as to the unique alleles described in this invention. As explained above, in any crosses between *Tripsacum* and teosinte, whether *Tripsacum* is the female parent or pollen donor in the cross, and regardless of which *Tripsacum* sp. is used in the cross, the precise genomic rearrangements that produce the novel recombinant alleles in progeny from said crosses occur. The replicability, genomic stability, and reliable heritability of these novel alleles have been demonstrated in crosses between different *Tripsacum* and teosinte parents from different plant populations and geographical regions (progeny from different crosses in which teosinte was the female parent and in which the parents came from divergent populations and different *Tripsacum* species are described on pages 22-23 and 24-29 and in Tables 3 and 4 of the specification). Because these novel alleles defy everything we know about mutations, mutation frequencies, and heritability in siblings (see detailed discussion above and in the specification, pages 2-3 and page 20), it would **not** have been obvious to, or anticipated by, anyone one skilled in the art that a high frequency of novel recombinant alleles (i.e. mutations not found in either parent) would occur in progeny derived from crossing *Tripsacum* and teosinte. Nor would it have been obvious to or anticipated by anyone skilled in the art that the same novel recombinant alleles (i.e. mutations not found in either parent) would occur in progeny from crossing different *Tripsacum* sp. and teosinte plants from different populations and geographical regions. This is unprecedented in the literature, defies the conventional paradigm for allelic inheritance in genetics, and clearly establishes that the prior art would neither anticipate nor render obvious the claimed invention.

In accordance with M.P.E.P. Section 1504.06 concerning non-statutory, obviousness double patenting, differences must be obvious to a designer of ordinary skill in the art related to the claimed design. If the reference does not fully disclose the narrower claim then a double-patenting rejection should not be made. "If the broader claim of the reference does not disclose the additional subject matter claimed in the narrower claim, then the applicant could not have claimed the narrower claim at the time the application with the broader claim was filed and a

rejection under non-statutory double patenting of the differing scope-type would be inappropriate." (http://www.bitlaw.com/source/mpep/1504_06.html)

Claim 23 has been amended according to the Examiner's recommendation such that steps described in Eubanks (U.S. Patent 5,750,828) are no longer in the amended claim and the prior art rejection is no longer applicable. Resistance to corn rootworm and lodging, which were claimed in Eubanks (U.S. Patent 5,750,828), are not claimed in this application.

(6) New Claims Rejections – 35 USC § 103(a)

Claim 23 was rejected under 35 U.S.C. 103(a) as being unpatentable over Eubanks (US Patent No. 5,330,547, July 19, 1994), in view of Gardiner et al. (*Genetics* 134:917-930, 1993). It should be noted that Eubanks US Patent No. 5,330,547 was filed on September 14, 1992, and predates the Gardiner et al. 1993 publication. This rejection fails to distinguish the unprecedented nature of the new genetic material upon which this application is based and the claims herein are drawn from Gardiner et al.'s work constructing an RFLP molecular map in maize. The specification describes a series of novel alleles formed in intergeneric hybrids between *Tripsacum* sp. and teosinte, said novel alleles (i.e. mutations) identified by their unique molecular weights and specific RFLP probe-restriction enzyme combinations. Gardiner et al. (1993, p. 918) characterized some of the RFLP probes, all of which are publicly available, for allelic variation in nine maize inbreds. In maize, these markers (i.e. probes) detect three or four alleles (i.e. polymorphisms) at each genetic locus in an easily interpretable pattern across a variety of inbred lines (Gardiner et al. 1993, p. 925). Development of the maize RFLP map took years of extensive experimentation by many researchers mapping multiple generations of populations of crosses between different inbred lines. Construction of the map was possible because each maize parent contributes the same parental allele per locus to the hybrid progeny produced by crossing two inbred lines. This invention is completely different, unobvious, and unprecedented because allelelic inheritance does not follow the basic premise of Gardiner et al. **Rather than inheriting an allele from each parent, the progeny of crosses between *Tripsacum* and teosinte exhibit novel alleles formed by intergeneric recombination between the distinctive genomes of *Tripsacum* and teosinte.** These novel alleles are visualized as bands on autoradiographs and are precisely described by their molecular weight and specific probe-enzyme combination. As stated in the specification, page 20, paragraph 1, "Such mutant or

novel rearrangements in the genetic material are revealed by comparative analysis of the RFLP bands of the parent plants and hybrid progeny. Bands present in the offspring not found in either parent indicate regions of the genome where novel genetic material has arisen, i.e. mutations have occurred...In addition to the rarity and usual deleterious effect of mutations, a basic biological tenet is that mutations occur at random or by chance (Lewin 1997). In a study of spontaneous mutation rates to new length alleles at tandemly repeated loci in human DNA (Jeffreys et al. 1988) mutations arose sporadically and there was no clustering of mutations within a family. Siblings never shared a common mutant allele. Therefore, it is unexpected that the same unique polymorphisms would be repeatedly found in hybrid progeny derived from crossing different *Tripsacum* and different teosinte parent plants..." This is unprecedented in the literature, defies the conventional paradigm for allelic inheritance in genetics, and clearly establishes that the prior art would neither anticipate nor render obvious the claimed invention.

Gardiner et al. (1993) provide a way to construct a molecular map based on statistical analyses of inheritance of alleles from each parent as they segregate in an immortalized F_2 mapping population and subsequent generations descended from the founders of the mapping population. The findings reported in this invention run counter to the basic premise upon which Gardiner et al. (1993) is based because the novel recombinant alleles formed by the intergeneric cross are not found in the parents and thus represent mutant genetic material. The recurring formation of the same novel alleles, i.e. mutations, indicates that these mutations do not occur at random or by chance as conventional genetic dogma holds. The unexpected discovery of this invention permits a new method of genetic analysis that can easily and rapidly detect a novel allele inherited from a *Tripsacum*-teosinte recombinant in maize. It also illustrates how to detect a novel allele in association with a trait in a small population from a single generation by simply comparing the novel genomic profiles of recombinants that express the trait with ones that do not. This invention is drawn to completely different subject matter that is distinct from construction of the maize RFLP map according to Gardiner et al. (1993). Therefore, the prior art rejection re Gardiner et al. (1993) is inappropriate and should be withdrawn.

In the Conclusion section, page 12, under item 14, of the Office Action, dated June 6, 2006, the Examiner stated that "Claims 13, 16, 17, 18, 19, 20, and 22 are deemed free of prior art given the failure of the prior art to teach or suggest a maize plant that contains one or more restriction fragments, produced by crossing a *Tripsacum*/teosinte hybrid with a maize plant, and

wherein the hybrid from said cross is distinguished by the presence of…" the traits designated in each of those claims. For the Examiner's convenience, it is noted that the claims previously deemed free of prior art correspond to currently amended claims as follows: claim 13 corresponds to claim 32; claim 16 corresponds to claim 28; claim 17 corresponds to claim 29; claim 18 corresponds to claim 30; claim 19 corresponds to claim 31, and claim 22 corresponds to claim 37.

The claims have been amended according to the Examiner's recommendations. The currently amended claims, along with the above responses to the wording informalities, obviousness-type double patenting, written description, enablement, and prior art rejections, are intended to clarify content and bring the application into proper order for allowance of the claims. A clean copy of the claims is included for the Examiner's convenience.

Respectfully submitted,

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